#9

SEQUENCE LISTING

<110> Kalluri, Raghuram

<120> ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE THEREOF

<130> 2312/2082B (formerly 1440.1027-016)

<140> US 10/032,221
<141> 2001-12-21

<150> PCT/US01/00565
<151> 2001-01-08

<150> US 09/625,191
<151> 2000-07-21

<150> US 09/543,371
<151> 2000-04-04

<150> US 09/479,118
<151> 2000-01-07

<150> US 09/335,224
<151> 1999-06-17

<150> US 60/126,175
<151> 1999-03-25

<150> US 60/089,689
<151> 1998-06-17

<160> 58

<170> PatentIn version 3.1

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<400> 1

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gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac tct       96
Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
            20                  25                  30

ttg ctc tac gtg caa ggc aat gaa cgg gcc cat gga cag gac ttg ggc      144
Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
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        35                  40                  45

acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg ttc      192
Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
    50                  55                  60

tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac tcg      240
Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
65                  70                  75                  80

tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc atc      288
Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
                85                  90                  95

acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt gag      336
Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
            100                 105                 110

gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc cca      384
Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
        115                 120                 125

ccg tgc ccc agc ggg tgg tcc tcg ctg tgg atc ggc tac tct ttt gtg      432
Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
    130                 135                 140

atg cac acc agc gct ggt gca gaa ggc tct ggc caa gcc ctg gcg tcc      480
Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
145                 150                 155                 160

ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag tgt      528
Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
                165                 170                 175

cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt tgg      576
His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
            180                 185                 190

ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg tcc      624
Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
        195                 200                 205

acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa gtc      672
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Cys Met Arg Arg Thr
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<210> 2
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<212> PRT
<213> Homo sapiens

<400> 2

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Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
            20                  25                  30

Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
        35                  40                  45

Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
    50                  55                  60

Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
65                  70                  75                  80

Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
                85                  90                  95

Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
            100                 105                 110

Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
        115                 120                 125

Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
    130                 135                 140

Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
145                 150                 155                 160

Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
                165                 170                 175

His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
            180                 185                 190

Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
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Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
    210                 215                 220
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Cys Met Arg Arg Thr
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ccc atg tgc ccg gtg ggc atg aac aaa ctc tgg agt gga tac agc ctg 96
Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
20 25 30

ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg 144
Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
35 40 45

gcg ggc tcc tgc ctg gcg cgg ttc agc acc atg ccc ttc ctg tac tgc 192
Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
50 55 60

aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac 240
Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr

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65                  70                  75                  80

tgg ctc tct acc act gcg ccg ctg ccc atg atg ccc gtg gcc gag gac      288
Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
                85                  90                  95

gag atc aag ccc tac atc agc cgc tgt tct gtg tgt gag gcc ccg gcc      336
Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
            100                 105                 110

atc gcc atc gcg gtc cac agt cag gat gtc tcc atc cca cac tgc cca      384
Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
        115                 120                 125

gct ggg tgg cgg agt ttg tgg atc gga tat tcc ttc ctc atg cac acg      432
Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
    130                 135                 140

gcg gcg gga gac gaa ggc ggt ggc caa tca ctg gtg tca ccg ggc agc      480
Ala Ala Gly Asp Glu Gly Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
145                 150                 155                 160

tgt cta gag gac ttc cgc gcc aca cca ttc atc gaa tgc aat gga ggc      528
Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
                165                 170                 175

cgc ggc acc tgc cac tac tac gcc aac aag tac agc ttc tgg ctg acc      576
Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
            180                 185                 190

acc att ccc gag cag agc ttc cag ggc tcg ccc tcc gcc gac acg ctc      624
Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
        195                 200                 205

aag gcc ggc ctc atc cgc aca cac atc agc cgc tgc cag gtg tgc atg      672
Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
    210                 215                 220

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Lys Asn Leu
225
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<210> 6
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<213> Homo sapiens

<400> 6

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Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
            20                  25                  30
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Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
35 40 45

Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
50 55 60

Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
65 70 75 80

Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
85 90 95

Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
100 105 110

Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
115 120 125

Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
130 135 140

Ala Ala Gly Asp Glu Gly Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
145 150 155 160

Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
165 170 175

Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
180 185 190

Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
195 200 205

Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
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Lys Asn Leu
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<220>
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<213> Homo sapiens

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acg aga ggc ttt gtc ttc acc cga cac agt caa acc aca gca att cct 96
Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile Pro
20 25 30

tca tgt cca gag ggg aca gtg cca ctc tac agt ggg ttt tct ttt ctt 144
Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
35 40 45

ttt gta caa gga aat caa cga gcc cac gga caa gac ctt gga act ctt 192
Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
50 55 60

ggc agc tgc ctg cag cga ttt acc aca atg cca ttc tta ttc tgc aat 240
Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
65 70 75 80

gtc aat gat gta tgt aat ttt gca tct cga aat gat tat tca tac tgg 288
Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
85 90 95

ctg tca aca cca gct ctg atg cca atg aac atg gct ccc att act ggc 336
Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly

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            100                 105                 110

aga gcc ctt gag cct tat ata agc aga tgc act gtt tgt gaa ggt cct      384
Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
        115                 120                 125

gcg atc gcc ata gcc gtt cac agc caa acc act gac att cct cca tgt      432
Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys
    130                 135                 140

cct cac ggc tgg att tct ctc tgg aaa gga ttt tca ttc atc atg ttc      480
Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe
145                 150                 155                 160

aca agt gca ggt tct gag ggc acc ggg caa gca ctg gcc tcc cct ggc      528
Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly
                165                 170                 175

tcc tgc ctg gaa gaa ttc cga gcc agc cca ttt cta gaa tgt cat gga      576
Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly
            180                 185                 190

aga gga acg tgc aac tac tat tca aat tcc tac agt ttc tgg ctg gct      624
Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala
        195                 200                 205

tca tta aac cca gaa aga atg ttc aga aag cct att cca tca act gtg      672
Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val
    210                 215                 220

aaa gct ggg gaa tta gaa aaa ata ata agt cgc tgt cag gtg tgc atg      720
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Lys Lys Arg His
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<210> 10
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<213> Homo sapiens

<400> 10

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Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
        35                  40                  45
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Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
50 55 60

Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
65 70 75 80

Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
85 90 95

Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly
100 105 110

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
115 120 125

Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys
130 135 140

Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe
145 150 155 160

Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly
165 170 175

Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly
180 185 190

Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala
195 200 205

Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val
210 215 220

Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met
225 230 235 240

Lys Lys Arg His

<210> 11
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<210> 12
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<223> primer

<400> 12
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<210> 13
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Additional vector sequence added to protein

<400> 13

Met Asp Ile Gly Ile Asn Ser Asp
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<210> 14
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Additional vector sequence added to protein

<400> 14

Lys Leu Ala Ala Ala Leu Glu
1 5

<210> 15
<211> 28
<212> DNA

<213> Artificial sequence

<220>
<223> pPICZaA forward oligonucleotide primer for Arresten

<400> 15
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<210> 16
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> pPICZaA reverse oligonucleotide primer for Arresten

<400> 16
tgctctagag gtgttcttct catacagact tggca 35

<210> 17
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> pPICZaA forward oligonucleotide primer for Canstatin

<400> 17
ttcggaattc gtcagcatcg gctacctcct g 31

<210> 18
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> pPICZaA reverse oligonucleotide primer for Canstatin

<400> 18
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<210> 19
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<212> PRT
<213> Artificial Sequence

<220>
<223> Deleted Sequence

<400> 19

Pro
1

<210> 20
<211> 124
<212> PRT
<213> Artificial Sequence

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<223> Tumstatin 333 (amino acids 1-124 of SEQ ID NO:10)

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Gly Leu Lys Gly Lys Arg Gly Asp Ser Gly Ser Pro Ala Thr Trp Thr
1 5 10 15

Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile Pro
20 25 30

Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
35 40 45

Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
50 55 60

Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
65 70 75 80

Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
85 90 95

Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly
100 105 110

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val
115 120

<210> 21
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Tumstatin 334 (amino acids 125-244 of SEQ ID NO:10)

<400> 21

Cys Glu Gly Pro Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp
1 5 10 15

Ile Pro Pro Cys Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser
20 25 30

Phe Ile Met Phe Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu
35 40 45

Ala Ser Pro Gly Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu
50 55 60

Glu Cys His Gly Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser
65 70 75 80

Phe Trp Leu Ala Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile
85 90 95

Pro Ser Thr Val Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys
100 105 110

Gln Val Cys Met Lys Lys Arg His
115 120

<210> 22
<211> 191
<212> PRT
<213> Artificial Sequence

<220>
<223> Tum-1 (Tumstatin N-53) (amino acids 54-244 of SEQ ID NO:10)

<400> 22

Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu Gly Ser Cys Leu Gln
1 5 10 15

Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp Val Cys
20 25 30

Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp Leu Ser Thr Pro Ala
35 40 45

Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly Arg Ala Leu Glu Pro
50 55 60

Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro Ala Ile Ala Ile Ala
65 70 75 80

Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys Pro His Gly Trp Ile
85 90 95

Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe Thr Ser Ala Gly Ser
100 105 110

Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly Ser Cys Leu Glu Glu
115 120 125

Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly Arg Gly Thr Cys Asn
130 135 140

Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala Ser Leu Asn Pro Glu
145 150 155 160

Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val Lys Ala Gly Glu Leu
165 170 175

Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met Lys Lys Arg His
180 185 190

<210> 23
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Tum-2 (amino acids 1-132 of SEQ ID NO:10)

<400> 23

Gly Leu Lys Gly Lys Arg Gly Asp Ser Gly Ser Pro Ala Thr Trp Thr
1 5 10 15

Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile Pro
20 25 30

Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
35 40 45

Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
50 55 60

Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn

65 70 75 80

Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
85 90 95

Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly
100 105 110

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
115 120 125

Ala Ile Ala Ile
130

<210> 24
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Tum-3 (amino acids 133-244 of SEQ ID NO:10)

<400> 24

Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys Pro His Gly Trp
1 5 10 15

Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe Thr Ser Ala Gly
20 25 30

Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly Ser Cys Leu Glu
35 40 45

Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly Arg Gly Thr Cys
50 55 60

Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala Ser Leu Asn Pro
65 70 75 80

Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val Lys Ala Gly Glu
85 90 95

Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met Lys Lys Arg His
100 105 110

<210> 25
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Tum-4 (amino acids 181-244 of SEQ ID NO:10)

<400> 25

Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly Arg Gly Thr Cys
1 5 10 15

Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala Ser Leu Asn Pro
20 25 30

Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val Lys Ala Gly Glu
35 40 45

Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met Lys Lys Arg His
50 55 60

<210> 26
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
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<400> 26

Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu Gly Ser Cys Leu Gln
1 5 10 15

Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp Val Cys
20 25 30

Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp Leu Ser Thr Pro Ala
35 40 45

Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly Arg Ala Leu Glu Pro
50 55 60

Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro Ala Ile Ala Ile
65 70 75

<210> 27

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> T1 (amino acids 1-19 of SEQ ID NO:10)

<400> 27

Gly Leu Lys Gly Lys Arg Gly Asp Ser Gly Ser Pro Ala Thr Trp Thr
1 5 10 15

Thr Arg Gly

<210> 28
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> T2 (amino acids 53-72 of SEQ ID NO:10)

<400> 28

Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu Gly Ser Cys Leu
1 5 10 15

Gln Arg Phe Thr
20

<210> 29
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> T3 (amino acids 68-87 of SEQ ID NO:10)

<400> 29

Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp
1 5 10 15

Val Cys Asn Phe
20

<210> 30
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> T4 (amino acids 83-102 of SEQ ID NO:10)

<400> 30

Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp Leu Ser
1 5 10 15

Thr Pro Ala Leu
20

<210> 31
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> T5 (amino acids 98-116 of SEQ ID NO:10)

<400> 31

Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly Arg
1 5 10 15

Ala Leu Glu

<210> 32
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> T6 (amino acids 113-131 of SEQ ID NO:10)

<400> 32

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
1 5 10 15

Ala Ile Ala

<210> 33
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Tumstatin-45-132 (amino acids 45-132 of SEQ ID NO:10)

<400> 33

Phe Ser Phe Leu Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp
1 5 10 15

Leu Gly Thr Leu Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe
20 25 30

Leu Phe Cys Asn Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp
35 40 45

Tyr Ser Tyr Trp Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala
50 55 60

Pro Ile Thr Gly Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val
65 70 75 80

Cys Glu Gly Pro Ala Ile Ala Ile
85

<210> 34
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> Tumstatin-5-125-C-A (amino acids 45-132 of SEQ ID NO:10; alanine has been substituted for the cysteine residue at position 125 of the full-length Tumstatin molecule)

<400> 34

Phe Ser Phe Leu Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp
1 5 10 15

Leu Gly Thr Leu Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe
20 25 30

Leu Phe Cys Asn Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp
35 40 45

Tyr Ser Tyr Trp Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala
50 55 60

Pro Ile Thr Gly Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val
65 70 75 80

Ala Glu Gly Pro Ala Ile Ala Ile
85

<210> 35
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic blocking peptide

<400> 35

Cys Asp Cys Arg Gly Asp Cys Phe Cys
1 5

<210> 36
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic blocking peptide

<400> 36

Cys Asn Gly Arg Cys
1 5

<210> 37
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> T7 (amino acids 73-97 of SEQ ID NO:10)

<400> 37

Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp Val Cys Asn Phe Ala
1 5 10 15

Ser Arg Asn Asp Tyr Ser Tyr Trp Leu
20 25

<210> 38
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> T7-mutant (amino acids 73-97 of SEQ ID NO:10; methionine has been substituted for the leucine residue at position 77 of the full-length Tumstatin molecule, and isoleucine has been substituted for valine at position 81, and asparagine has been substituted for a spartic acid at position 83)

<400> 38

Thr Met Pro Phe Met Phe Cys Asn Ile Asn Asn Val Cys Asn Phe Ala
1 5 10 15

Ser Arg Asn Asp Tyr Ser Tyr Trp Leu
20 25

<210> 39
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> T8 (amino acids 68-94 of SEQ ID NO:10; lysine has been substituted for the leucine residue at position 68 of the full-length Tumstatin molecule)

<400> 39

Lys Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp
1 5 10 15

Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
20 25

<210> 40
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> T8-3 (amino acids 68-94 of SEQ ID NO:10; lysine has been substituted for the leucine residue at position 68 of the full-length Tumstatin molecule, and serine has been substituted for the cysteine residues at positions 79 and 85)

<400> 40

Lys Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Ser Asn Val Asn Asp
1 5 10 15

Val Ser Asn Phe Ala Ser Arg Asn Asp Tyr Ser
20 25

<210> 41
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> TP3 (amino acids 76-94 of SEQ ID NO:10; lysine has been substitut
ed for the phenylalanine residue at position 76 of the full-lengt
h Tumstatin molecule, and cysteine has been substituted for the
aspartic acid at position 83)

<400> 41

Lys Leu Phe Cys Asn Val Asn Cys Val Cys Asn Phe Ala Ser Arg Asn
1 5 10 15

Asp Tyr Ser

<210> 42
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> P2 (amino acids 68-94 of SEQ ID NO:10; lysine has been substitut
ed for the leucine residue at position 68 of the full-length Tums
tatin molecule, and aspartic acid has been substituted for the cy
steine residues at positions 79 and 85)

<400> 42

Lys Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Asp Asn Val Asn Asp
1 5 10 15

Val Asp Asn Phe Ala Ser Arg Asn Asp Tyr Ser
20 25

<210> 43
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Scrambled peptide SP1

<400> 43

Ala Asn Met Ser Arg Asn Val Phe Phe Asp Cys Thr Ser Phe Pro Val
1 5 10 15

Cys Gln Lys Phe Leu Asn Asp Thr Arg Asn Tyr
20 25

<210> 44
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Scrambled peptide SP2

<400> 44

Thr Phe Asn Cys Val Lys Asn Tyr Gln Arg Leu Asp Phe Thr Ser Arg
1 5 10 15

Phe Val Met Asp Ser Cys Ala Asn Phe Pro Asn
20 25

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic peptide

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa at position 1 is any amino acid

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa at position 2 is Phe or Lys

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa at position 5 is Cys, Ser or Asp

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa at position 9 is Asp or Cys

<220>
<221> MISC_FEATURE
<222> (11)..(11)

<223> Xaa at position 11 is Cys, Ser or Asp

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa at position 14 is any amino acid

<400> 45

Xaa Xaa Leu Phe Xaa Asn Val Asn Xaa Val Xaa Asn Phe Xaa
1 5 10

<210> 46
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 46

Thr Thr Met Pro
1

<210> 47
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 47

Phe Thr Thr Met Pro
1 5

<210> 48
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 48

Arg Phe Thr Thr Met Pro
1 5

<210> 49
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic peptide

<400> 49

Gln Arg Phe Thr Thr Met Pro
1 5

<210> 50
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 50

Leu Gln Arg Phe Thr Thr Met Pro
1 5

<210> 51
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 51

Lys Gln Arg Phe Thr Thr Met Pro
1 5

<210> 52
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 52

Ala Ser Arg Asn
1

<210> 53

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 53

Ala Ser Arg Asn Asp
1 5

<210> 54
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 54

Ala Ser Arg Asn Asp Tyr
1 5

<210> 55
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 55

Ala Ser Arg Asn Asp Tyr Ser
1 5

<210> 56
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 56

Ala Ser Arg Asn Asp Tyr Ser Tyr
1 5

<210> 57
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 57

Ala Ser Arg Asn Asp Tyr Asp Tyr Trp
1 5

<210> 58
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Generic Peptide

<400> 58

Ala Ser Arg Asn Asp Tyr Ser Tyr Trp Leu
1 5 10